Freeing protein-based drugs from bacteria's natural traps

October 13 2008

In a finding that could speed the development of new protein-based drugs for fighting diabetes, hepatitis, and other diseases, researchers are reporting progress toward preventing or destroying an unusual structure that reduces the production yield of bioengineered drugs. The article is scheduled for the Oct. 13 issue of Chemical & Engineering News, ACS' weekly newsmagazine.

In the article, C&EN Associate Editor Jyllian Kemsley notes that genetically-engineered E. coli bacteria are increasingly used to produce protein-based drugs for a variety of diseases.

However, these proteins are often not usable because they become trapped in large, insoluble clumps called "inclusion bodies." Current methods to extract proteins trapped in these clumps involve breaking down the clumps chemically and refolding the proteins, a process that is inefficient and sometimes destroys the desired protein.

In the article, Kemsley describes new research insights into the structure and formation of these unusual clumps that could lead to their prevention. Scientists, for instance, have discovered evidence that inclusion bodies form due to interactions between molecular structures called beta-sheets and that clumping could be prevented by preventing beta-sheet interactions.

Article: "Protein Aggregates Probed";
pubs.acs.org/cen/science/86/8641sci1.html

Source: ACS